

SEQUENCE LISTING

<110> Chau, Vincent
 <120> Human Proteins Responsible for NEDD8 Activation and Conjugation
 <130> 103576-127
 <140> US 09/216,430
 <141> 1998-12-18
 <150> PCT/US98/27141
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 <150> US 60/068,209
 <151> 1998-08-12
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 Trp Asn His Val Lys Lys Phe Leu Glu Arg Ser Gly Pro Phe Thr His
 20 25 30
 cct gat ttc gaa ccg agc act gaa tct ctc cag ttc ttg tta gat aca 144
 Pro Asp Phe Glu Pro Ser Thr Glu Ser Leu Gln Phe Leu Leu Asp Thr
 35 40 45
 tgt aaa gtt cta gtc att gga gct ggc ggc tta gga tgt gag ctc ctg 192
 Cys Lys Val Leu Val Ile Gly Ala Gly Gly Leu Gly Cys Glu Leu Leu
 50 55 60
 aaa aat ctg gcc ttg tct ggt ttt aga cag att cat gtt ata gat atg 240
 Lys Asn Leu Ala Leu Ser Gly Phe Arg Gln Ile His Val Ile Asp Met
 65 70 75 80

gac act ata gat gtt tcc aat cta aat agg cag ttt tta ttt agg cct Asp Thr Ile Asp Val Ser Asn Leu Asn Arg Gln Phe Leu Phe Arg Pro 85 90 95	288
aaa gat att gga aga cct aag gct gaa gtt gct gca gaa ttt cta aat Lys Asp Ile Gly Arg Pro Lys Ala Glu Val Ala Ala Glu Phe Leu Asn 100 105 110	336
gac aga gtt cct aat tgc aat gta gtt cca cat ttc aac aag att caa Asp Arg Val Pro Asn Cys Asn Val Val Pro His Phe Asn Lys Ile Gln 115 120 125	384
gat ttt aac gac act ttc tat cga caa ttt cat att att gta tgt gga Asp Phe Asn Asp Thr Phe Tyr Arg Gln Phe His Ile Ile Val Cys Gly 130 135 140	432
ctg gac tct atc atc gcc aga aga tgg ata aat ggc atg ctg ata tct Leu Asp Ser Ile Ile Ala Arg Arg Trp Ile Asn Gly Met Leu Ile Ser 145 150 155 160	480
ctt cta aat tat gaa gat ggt gtc tta gat cca agc tcc att gtc cct Leu Leu Asn Tyr Glu Asp Gly Val Leu Asp Pro Ser Ser Ile Val Pro 165 170 175	528
ttg ata gat ggg ggg aca gaa ggt ttt aaa gga aat gcc cgg gtg att Leu Ile Asp Gly Gly Thr Glu Gly Phe Lys Gly Asn Ala Arg Val Ile 180 185 190	576
ctg cct gga atg act gct tgt atc gaa tgc acg ctg gaa ctt tat cca Leu Pro Gly Met Thr Ala Cys Ile Glu Cys Thr Leu Glu Leu Tyr Pro 195 200 205	624
cca cag gtt aat ttt ccc atg tgc acc att gca tct atg ccc agg cta Pro Gln Val Asn Phe Pro Met Cys Thr Ile Ala Ser Met Pro Arg Leu 210 215 220	672
cca gaa cac tgt att gag tat gta agg atg ttg cag tgg cct aag gag Pro Glu His Cys Ile Glu Tyr Val Arg Met Leu Gln Trp Pro Lys Glu 225 230 235 240	720
cag cct ttt gga gaa ggg gtt cca tta gat aga gat gat cct gaa cat Gln Pro Phe Gly Glu Gly Val Pro Leu Asp Arg Asp Asp Pro Glu His 245 250 255	768
ata caa tgg att ttc caa aaa tcc cta gag aga gca tca caa tat aat Ile Gln Trp Ile Phe Gln Lys Ser Leu Glu Arg Ala Ser Gln Tyr Asn 260 265 270	816
att agg ggt gtt acg tat agg ctc act caa ggg gta gta aaa aga atc Ile Arg Gly Val Thr Tyr Arg Leu Thr Gln Gly Val Val Lys Arg Ile 275 280 285	864
att cct gca gta gct tcc aca aat gca gtc att gca gct gtg tgt gcc Ile Pro Ala Val Ala Ser Thr Asn Ala Val Ile Ala Ala Val Cys Ala 290 295 300	912

act gag gtt ttt aaa ata gcc aca agt gca tac att ccc ttg aat aat 960
 Thr Glu Val Phe Lys Ile Ala Thr Ser Ala Tyr Ile Pro Leu Asn Asn
 305 310 315 320
 tac ttg gtg ttt aat gat gta gat ggg ctg tat aca tac aca ttt gaa 1008
 Tyr Leu Val Phe Asn Asp Val Asp Gly Leu Tyr Thr Tyr Thr Phe Glu
 325 330 335
 gca gaa aga aag gaa aac tgc cca gct tgt agc cag ctt cct caa aat 1056
 Ala Glu Arg Lys Glu Asn Cys Pro Ala Cys Ser Gln Leu Pro Gln Asn
 340 345 350
 att cag ttt tct cca tca gct aaa cta cag gag gtt ttg gat tat cta 1104
 Ile Gln Phe Ser Pro Ser Ala Lys Leu Gln Glu Val Leu Asp Tyr Leu
 355 360 365
 acc aat agt gct tct ctg caa atg aaa tct cca gcc atc aca gcc acc 1152
 Thr Asn Ser Ala Ser Leu Gln Met Lys Ser Pro Ala Ile Thr Ala Thr
 370 375 380
 cta gag gga aaa aat aga aca ctt tac tta cag tcg gta acc tct att 1200
 Leu Glu Gly Lys Asn Arg Thr Leu Tyr Leu Gln Ser Val Thr Ser Ile
 385 390 395 400
 gaa gaa cga aca agg cca aat ctc tcc aaa aca ttg aaa gaa ttg ggg 1248
 Glu Glu Arg Thr Arg Pro Asn Leu Ser Lys Thr Leu Lys Glu Leu Gly
 405 410 415
 ctt gtt gat gga caa gaa ctg gcg gtt gct gat gtc acc acc cca cag 1296
 Leu Val Asp Gly Gln Glu Leu Ala Val Ala Asp Val Thr Thr Pro Gln
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Pro Asn Phe Glu Pro Ser Thr Glu Ser Leu Gln Phe Leu Leu Asp Thr
 35 40 45

Cys Lys Val Leu Val Ile Gly Ala Gly Gly Leu Gly Cys Glu Leu Leu
 50 55 60

Lys Asn Leu Ala Leu Ser Gly Phe Arg Gln Ile His Val Ile Asp Met
 65 70 75 80

Asp Thr Ile Asp Val Ser Asn Leu Asn Arg Gln Phe Leu Phe Arg Pro
 85 90 95

Lys Asp Ile Gly Arg Pro Lys Ala Glu Val Ala Ala Glu Phe Leu Asn
 100 105 110

Asp Arg Val Pro Asn Cys Asn Val Val Pro His Phe Asn Lys Ile Gln
 115 120 125

Asp Phe Asn Asp Thr Phe Tyr Arg Gln Phe His Ile Ile Val Cys Gly
 130 135 140

Leu Asp Ser Ile Ile Ala Arg Arg Trp Ile Asn Gly Met Leu Ile Ser
 145 150 155 160

Leu Leu Asn Tyr Glu Asp Gly Val Leu Asp Pro Ser Ser Ile Val Pro
 165 170 175

Leu Ile Asp Gly Gly Thr Glu Gly Phe Lys Gly Asn Ala Arg Val Ile
 180 185 190

Leu Pro Gly Met Thr Ala Cys Ile Glu Cys Thr Leu Glu Leu Tyr Pro
 195 200 205

Pro Gln Val Asn Phe Pro Met Cys Thr Ile Ala Ser Met Pro Arg Leu
 210 215 220

Pro Glu His Cys Ile Glu Tyr Val Arg Met Leu Gln Trp Pro Lys Glu
 225 230 235 240

Gln Pro Phe Gly Glu Gly Val Pro Leu Asp Arg Asp Asp Pro Glu His
 245 250 255

Ile Gln Trp Ile Phe Gln Lys Ser Leu Glu Arg Ala Ser Gln Tyr Asn
 260 265 270

Ile Arg Gly Val Thr Tyr Arg Leu Thr Gln Gly Val Val Lys Arg Ile
 275 280 285

Ile Pro Ala Val Ala Ser Thr Asn Ala Val Ile Ala Ala Val Cys Ala
 290 295 300

Thr Glu Val Phe Lys Ile Ala Thr Ser Ala Tyr Ile Pro Leu Asn Asn
 305 310 315 320

Tyr Leu Val Phe Asn Asp Val Asp Gly Leu Tyr Thr Tyr Thr Phe Glu
 325 330 335

Ala Glu Arg Lys Glu Asn Cys Pro Ala Cys Ser Gln Leu Pro Gln Asn
 340 345 350

Ile Gln Phe Ser Pro Ser Ala Lys Leu Gln Glu Val Leu Asp Tyr Leu
 355 360 365

Thr Asn Ser Ala Ser Leu Gln Met Lys Ser Pro Ala Ile Thr Ala Thr
 370 375 380

Leu Glu Gly Lys Asn Arg Thr Leu Tyr Leu Gln Ser Val Thr Ser Ile
 385 390 395 400

Glu Glu Arg Thr Arg Pro Asn Leu Ser Lys Thr Leu Lys Glu Leu Gly
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Thr Val Leu Phe Lys Leu His Phe Thr Ser
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gcg ggc ggc acc aag ggc agc agc aag aag gcg tcg gcg gcg cag ctg	96
Ala Gly Gly Thr Lys Gly Ser Ser Lys Lys Ala Ser Ala Ala Gln Leu	
20 25 30	
cgg atc cag aag gac ata aac gag ctg aac ctg ccc aag acg tgt gat	144
Arg Ile Gln Lys Asp Ile Asn Glu Leu Asn Leu Pro Lys Thr Cys Asp	
35 40 45	
atc agc ttc tca gat cca gac gac ctc ctc aac ttc aag ctg gtc atc	192
Ile Ser Phe Ser Asp Pro Asp Asp Leu Leu Asn Phe Lys Leu Val Ile	
50 55 60	
tgt cct gat gag ggc ttc tac aag agt ggg aag ttt gtg ttc agt ttt	240
Cys Pro Asp Glu Gly Phe Tyr Lys Ser Gly Lys Phe Val Phe Ser Phe	
65 70 75 80	
aag gtg ggc cag ggt tac ccg cat gat ccc ccc aag gtg aag tgt gag	288
Lys Val Gly Gln Gly Tyr Pro His Asp Pro Pro Lys Val Lys Cys Glu	
85 90 95	
aca atg gtc tat cac ccc aac att gac ctc gag ggc aac gtc tgc ctc	336
Thr Met Val Tyr His Pro Asn Ile Asp Leu Glu Gly Asn Val Cys Leu	
100 105 110	
aac atc ctc aga gag gac tgg aag cca gtc ctt acg ata aac tcc ata	384
Asn Ile Leu Arg Glu Asp Trp Lys Pro Val Leu Thr Ile Asn Ser Ile	
115 120 125	
att tat ggc ctg cag tat ctc ttc ttg gag ccc aac ccc gag gac cca	432
Ile Tyr Gly Leu Gln Tyr Leu Phe Leu Glu Pro Asn Pro Glu Asp Pro	
130 135 140	
ctg aac aag gag gcc gca gag gtc ctg cag aac aac cgg cgg ctg ttt	480
Leu Asn Lys Glu Ala Ala Glu Val Leu Gln Asn Asn Arg Arg Leu Phe	
145 150 155 160	
gag cag aac gtg cag cgc tcc atg cgg ggt ggc tac atc ggc tcc acc	528
Glu Gln Asn Val Gln Arg Ser Met Arg Gly Gly Tyr Ile Gly Ser Thr	
165 170 175	
tac ttt gag cgc tgc ctg aaa tag	552
Tyr Phe Glu Arg Cys Leu Lys	
180	

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Ala Gly Gly Thr Lys Gly Ser Ser Lys Lys Ala Ser Ala Ala Gln Leu
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Arg Ile Gln Lys Asp Ile Asn Glu Leu Asn Leu Pro Lys Thr Cys Asp
 35 40 45

Ile Ser Phe Ser Asp Pro Asp Asp Leu Leu Asn Phe Lys Leu Val Ile
 50 55 60

Cys Pro Asp Glu Gly Phe Tyr Lys Ser Gly Lys Phe Val Phe Ser Phe
 65 70 75 80

Lys Val Gly Gln Gly Tyr Pro His Asp Pro Pro Lys Val Lys Cys Glu
 85 90 95

Thr Met Val Tyr His Pro Asn Ile Asp Leu Glu Gly Asn Val Cys Leu
 100 105 110

Asn Ile Leu Arg Glu Asp Trp Lys Pro Val Leu Thr Ile Asn Ser Ile
 115 120 125

Ile Tyr Gly Leu Gln Tyr Leu Phe Leu Glu Pro Asn Pro Glu Asp Pro
 130 135 140

Leu Asn Lys Glu Ala Ala Glu Val Leu Gln Asn Asn Arg Arg Leu Phe
 145 150 155 160

Glu Gln Asn Val Gln Arg Ser Met Arg Gly Gly Tyr Ile Gly Ser Thr
 165 170 175

Tyr Phe Glu Arg Cys Leu Lys
180

<210> 5
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tcc cgg acg gca gcc aca gcg tcc gac tcg act cgg agg gtt tct gtg 96
Ser Arg Thr Ala Ala Thr Ala Ser Asp Ser Thr Arg Arg Val Ser Val
20 25 30

aga gac aaa ttg ctt gtt aaa gag gtt gca gaa ctt gaa gct aat tta 144
Arg Asp Lys Leu Leu Val Lys Glu Val Ala Glu Leu Glu Ala Asn Leu
35 40 45

cct tgt aca tgt aaa gtg cat ttt cct gat cca aac aag ctt cat tgt 192
Pro Cys Thr Cys Lys Val His Phe Pro Asp Pro Asn Lys Leu His Cys
50 55 60

ttt cag cta aca gta acc cca gat gag ggt tac tac cag ggt gga aaa 240
Phe Gln Leu Thr Val Thr Pro Asp Glu Gly Tyr Tyr Gln Gly Gly Lys
65 70 75 80

ttt cag ttt gaa act gaa gtt ccc gat gcg tac aac atg gtg cct ccc 288
Phe Gln Phe Glu Thr Glu Val Pro Asp Ala Tyr Asn Met Val Pro Pro
85 90 95

aaa gtg aaa tgc ctg acc aag atc tgg cac ccc aac atc aca gag aca 336
Lys Val Lys Cys Leu Thr Lys Ile Trp His Pro Asn Ile Thr Glu Thr
100 105 110

ggg gaa ata tgt ctg agt tta ttg aga gaa cat tca att gat ggc act 384
Gly Glu Ile Cys Leu Ser Leu Leu Arg Glu His Ser Ile Asp Gly Thr
115 120 125

ggc tgg gct ccc aca aga aca tta aag gat gtc gtt tgg gga tta aac 432
Gly Trp Ala Pro Thr Arg Thr Leu Lys Asp Val Val Trp Gly Leu Asn
130 135 140

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tct ttg ttt act gat ctt ttg aat ttt gat gat cca ctg aat att gaa      480
Ser Leu Phe Thr Asp Leu Leu Asn Phe Asp Asp Pro Leu Asn Ile Glu
145                      150                      155                      160

gct gca gaa cat cat ttg cgg gac aag gag gac ttc cgg aat aaa gtg      528
Ala Ala Glu His His Leu Arg Asp Lys Glu Asp Phe Arg Asn Lys Val
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gat gac tac atc aaa cgt tat gcc aga tga      558
Asp Asp Tyr Ile Lys Arg Tyr Ala Arg
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Ser Arg Thr Ala Ala Thr Ala Ser Asp Ser Thr Arg Arg Val Ser Val
                      20                      25                      30

Arg Asp Lys Leu Leu Val Lys Glu Val Ala Glu Leu Glu Ala Asn Leu
35                      40                      45

Pro Cys Thr Cys Lys Val His Phe Pro Asp Pro Asn Lys Leu His Cys
50                      55                      60

Phe Gln Leu Thr Val Thr Pro Asp Glu Gly Tyr Tyr Gln Gly Gly Lys
65                      70                      75                      80

Phe Gln Phe Glu Thr Glu Val Pro Asp Ala Tyr Asn Met Val Pro Pro
85                      90                      95

Lys Val Lys Cys Leu Thr Lys Ile Trp His Pro Asn Ile Thr Glu Thr
100                      105                      110

Gly Glu Ile Cys Leu Ser Leu Leu Arg Glu His Ser Ile Asp Gly Thr
115                      120                      125

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Gly Trp Ala Pro Thr Arg Thr Leu Lys Asp Val Val Trp Gly Leu Asn
 130 135 140

Ser Leu Phe Thr Asp Leu Leu Asn Phe Asp Asp Pro Leu Asn Ile Glu
 145 150 155 160

Ala Ala Glu His His Leu Arg Asp Lys Glu Asp Phe Arg Asn Lys Val
 165 170 175

Asp Asp Tyr Ile Lys Arg Tyr Ala Arg
 180 185

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 ttcccgtcgt cgttcttccg cagccgccgc gtcgacgcct aggtcttcct gtatttgctc 120
 gacttggaag ggttctgcac actatagtcg aagagtctag gtctgctgga ggagttgaag 180
 ttcgaccagt agacaggact actccgaag atgttctcac ccttcaaaca caagtcaaaa 240
 ttccacccgg tcccaatggg cgtactaggg gggttccact tcacactctg ttaccagata 300
 gtgggggttg aactggagct cccgttgagc acggagttgt aggagtctct cctgaccttc 360
 ggtcaggaat gctatttgag gtattaaata ccggacgtca tagagaagaa cctcgggttg 420
 gggctcctgg gtgacttggt cctccggcgt ctccaggacg tcttggtggc cgccgacaaa 480
 ctcgtcttgc acgtcgcgag gtacgccccca ccgatgtagc cgaggtggat gaaactcgcg 540
 acgacttita tc 552

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Asn Ser Ser Ser Ile Gln Pro Asn Leu Ser Ala Ala Arg Ile Arg Leu
 20 25 30

Lys Arg Asp Leu Asp Ser Leu Asp Leu Pro Pro Thr Val Thr Leu Asn
 35 40 45

Val Ile Thr Ser Pro Asp Ser Ala Asp Arg Ser Gln Ser Pro Lys Leu
 50 55 60

Asn Val Cys Leu Asn Ile Leu Arg Glu Asp Trp Ser Pro Ala Leu Asp
 65 70 75 80

Leu Gln Ser Ile Ile Thr Gly Leu Leu Phe Leu Phe Leu Glu Pro Asn
 85 90 95

Pro Asn Asp Pro Leu Asn Lys Asp Ala Ala Lys Leu Leu Cys Glu Gly
 100 105 110

Glu Lys Glu Phe Ala Glu Ala Val Arg Leu Thr Met Ser Gly Gly Ser
 115 120 125

Ile Glu His Val Lys Tyr Asp Asn Ile Val Ser Pro
 130 135 140

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ttcgaagtaa caaaagtcga ttgtcattgg ggtctactcc caatgatggg cccacctttt 240
aaagtcaaac tttgacttca agggctacgc atgttgtagc acggagggtt tcactttacg 300
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tctcttgtaa gttaactacc gtgaccgacc cgagggtgtt cttgtaattt cctacagcaa 420
accctaatt tgagaaacaa atgactagaa aacttaaac tactaggtga cttataactt 480
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Tyr Leu Glu Thr Arg Ile Ala Val Arg Asp Lys Leu Leu Ala Gln Glu
20             25             30

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Leu Gln Gln Leu Glu Thr Ala Leu Arg Asp Gln Lys Gln Lys Leu Trp
35             40             45

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His Leu Glu Val Pro Ser Thr Ser Cys Leu His Glu Leu Glu Leu Thr
50             55             60

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Val Thr Pro Gln Glu Gly Ile Tyr Arg Gly Gly Lys Phe Arg Phe Lys
65             70             75             80

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Ile Thr Val Pro Pro Glu Tyr Asn Asn Val Pro Pro Val Val Lys Cys
85             90             95

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Leu Thr Lys Val Trp His Pro Asn Ile Asn Glu Asp Gly Ser Ile Cys
 100 105 110

Leu Ser Ile Leu Arg Gln Asn Ser Leu Asp Gln Tyr Gly Trp Arg Pro
 115 120 125

Thr Arg Asn Leu Thr Asp Val Val His Gly Leu Val Ser Leu Phe Asn
 130 135 140

Asp Leu Met Asp Phe Asn Asp Ala Leu Asn Ile Gln Ala Ala Gln Met
 145 150 155 160

Trp Ser Trp Asn Arg Glu Ser Phe Asn His Arg Val Arg Glu Tyr Ile
 165 170 175

Ser Arg Tyr Cys
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 20 25 30

Asp Glu Asn Phe Thr Glu Leu Arg Gly Glu Ile Ala Gly Pro Pro Asp
 35 40 45

Thr Pro Tyr Glu Gly Gly Arg Tyr Gln Leu Glu Ile Lys Ile Pro Glu
 50 55 60

Thr Tyr Pro Phe Asn Pro Pro Lys Val Arg Phe Ile Thr Lys Ile Trp
 65 70 75 80

His Pro Asn Ile Ser Ser Val Thr Gly Ala Ile Cys Leu Asp Leu Leu
 85 90 95

Lys Asp Gln Trp Ala Ala Ala Met Thr Leu Arg Thr Val Leu Leu Ser
 100 105 110

Leu Gln Ala Asp Leu Ala Ala Ala Glu Pro Asp Asp Pro Gln Asp Ala
 115 120 125

Val Val Ala Asn Gln Tyr Lys Gln Asn Pro Glu Met Phe Lys Gln Thr
 130 135 140

Ala Arg Leu Trp Ala His Val Tyr Ala Gly Ala Pro Val Ser Ser Pro
 145 150 155 160

Glu Tyr Thr Lys Lys Ile Glu Asn Leu Cys Ala Met Gly Phe Asp Arg
 165 170 175

Asn Ala Val Ile Val Ala Leu Ser Ser Lys Ser Trp Asp Val Glu Thr
 180 185 190

Ala Thr Glu Leu Leu Leu Ser Asn
 195 200

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Ile Met Gln Trp Asn Ala Val Ile Phe Gly Pro Glu Gly Thr Pro Phe
 35 40 45

Glu Asp Gly Thr Phe Lys Leu Val Ile Glu Phe Ser Glu Glu Tyr Pro
 50 55 60

Asn Lys Pro Pro Thr Val Arg Phe Val Ser Lys Met Phe His Pro Asn
 65 70 75 80

Val Tyr Ala Asp Gly Ser Ile Cys Leu Asp Ile Leu Gln Asn Arg Trp
 85 90 95

Ser Pro Thr Tyr Asp Val Ser Ser Ile Leu Thr Ser Ile Gln Ser Asp
 100 105 110

Leu Asp Glu Pro Asn Pro Asn Ser Pro Ala Asn Ser Gln Ala Ala Gln
 115 120 125

Leu Tyr Gln Glu Asn Lys Arg Glu Tyr Glu Lys Arg Val Ser Ala Ile
 130 135 140

Val Ile Gln Ser Trp Asn Asp Ser
 145 150

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 20 25 30

Ile Met Val Trp Asn Ala Val Ile Phe Gly Pro Glu Gly Thr Pro Phe
 35 40 45

Gly Asp Gly Thr Phe Lys Leu Thr Ile Glu Phe Thr Glu Glu Tyr Pro
 50 55 60

Asn Lys Pro Pro Thr Val Arg Phe Val Ser Lys Met Phe His Pro Asn
65 70 75 80

Val Tyr Ala Asp Gly Ser Ile Cys Leu Asp Ile Leu Gln Asn Arg Trp
85 90 95

Ser Pro Thr Tyr Asp Val Ser Ser Ile Leu Thr Ser Ile Gln Ser Asp
100 105 110

Leu Asp Glu Pro Asn Pro Asn Ser Pro Ala Asn Ser Gln Ala Ala Gln
115 120 125

Leu Tyr Gln Glu Asn Lys Arg Glu Tyr Glu Lys Arg Val Ser Ala Ile
130 135 140

Val Ile Gln Ser Trp Arg Asp Cys
145 150

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Met Ala Arg Pro Leu Val Pro Ser Ser Gln Lys Ala Leu Leu Leu Glu
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20 25 30

Val Asp Glu Gly Asp Leu Tyr Asn Trp Glu Val Ala Ile Phe Gly Pro
35 40 45

Pro Asn Thr Tyr Tyr Glu Gly Gly Tyr Phe Lys Ala Arg Leu Lys Phe
50 55 60

Pro Ile Asp Tyr Pro Tyr Ser Pro Pro Ala Phe Arg Phe Leu Thr Lys
65 70 75 80

Met Trp His Pro Asn Ile Tyr Glu Thr Gly Asp Val Cys Ile Ser Ile
85 90 95

Leu His Pro Pro Val Asp Asp Pro Gln Ser Gly Glu Leu Pro Ser Glu
100 105 110

Arg Trp Asn Pro Thr Gln Asn Val Arg Thr Ile Leu Leu Ser Val Ile
115 120 125

Ser Asp Leu Asn Glu Pro Asn Thr Phe Ser Pro Ala Asn Val Asp Ala
130 135 140

Ser Val Met Tyr Arg Lys Trp Lys Glu Ser Lys Gly Lys Asp Arg Glu
145 150 155 160

Tyr Thr Asp Ile Ile Arg Lys Gln Val Leu Gly Thr Lys Val Asp Ala
165 170 175

Glu Arg Asp Gly Val Lys Val Pro Thr Thr Leu Ala Glu Tyr Cys Val
180 185 190

Lys Thr Lys Ala Pro Ala Pro Asp Glu Gly Ser Asp Leu Phe Tyr Asp
195 200 205

Asp Tyr Tyr Glu Asp Gly Glu Val Glu Glu Glu Ala Asp Ser Cys Phe
210 215 220

Gly Asp Asp Glu Asp Asp Ser Gly Thr Glu Glu Ser
225 230 235

<210> 15
<211> 147
<212> PRT
<213> Human

<220>
<221> MISC_FEATURE
<222> (1)..(147)
<223> UBC5b

<400> 15

Met Ala Leu Lys Arg Ile His Lys Glu Leu Asn Asp Leu Ala Arg Asp
1 5 10 15

Pro Pro Ala Gln Cys Ser Ala Gly Pro Val Gly Asp Asp Met Phe His
 20 25 30

Trp Gln Ala Thr Ile Met Gly Pro Asn Asp Ser Pro Tyr Gln Gly Gly
 35 40 45

Val Phe Phe Leu Thr Ile His Phe Pro Thr Asp Tyr Pro Phe Lys Pro
 50 55 60

Pro Lys Val Ala Phe Thr Thr Arg Ile Tyr His Pro Asn Ile Asn Ser
 65 70 75 80

Asn Gly Ser Ile Cys Leu Asp Ile Leu Arg Ser Gln Trp Ser Pro Ala
 85 90 95

Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Asp Leu Cys Asp
 100 105 110

Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala Arg Ile Tyr Lys
 115 120 125

Thr Asp Arg Glu Lys Tyr Asn Arg Ile Ala Arg Glu Trp Thr Gln Lys
 130 135 140

Tyr Ala Met
 145

<210> 16
 <211> 147
 <212> PRT
 <213> Human

<220>
 <221> MISC_FEATURE
 <222> (1)..(147)
 <223> UBC5c

<400> 16

Met Ala Leu Lys Arg Ile Asn Lys Glu Leu Ser Asp Leu Ala Arg Asp
 1 5 10 15

Pro Pro Ala Gln Cys Ser Ala Gly Pro Val Gly Asp Asp Met Phe His
 20 25 30

Trp Gln Ala Thr Ile Met Gly Pro Asn Asp Ser Pro Tyr Gln Gly Gly
 35 40 45

Val Phe Phe Leu Thr Ile His Phe Pro Thr Asp Tyr Pro Phe Lys Pro
 50 55 60

Pro Lys Val Ala Phe Thr Thr Arg Ile Tyr His Pro Asn Ile Asn Ser
 65 70 75 80

Asn Gly Ser Ile Cys Leu Asp Ile Leu Arg Ser Gln Trp Ser Pro Ala
 85 90 95

Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Asp Leu Cys Asp
 100 105 110

Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala Arg Ile Tyr Lys
 115 120 125

Thr Asp Arg Asp Lys Tyr Asn Arg Ile Ser Arg Glu Trp Thr Gln Lys
 130 135 140

Tyr Ala Met
 145

<210> 17
 <211> 147
 <212> PRT
 <213> Human

<220>
 <221> MISC_FEATURE
 <222> (1)..(147)
 <223> UBC5a

<400> 17

Met Ala Leu Lys Arg Ile Gln Lys Glu Leu Ser Asp Leu Gln Arg Asp
 1 5 10 15

Pro Pro Ala His Cys Ser Ala Gly Pro Val Gly Asp Asp Leu Phe His
 20 25 30

Trp Gln Ala Thr Ile Met Gly Pro Pro Asp Ser Ala Tyr Gln Gly Gly
 35 40 45

Val Phe Phe Leu Thr Val His Phe Pro Thr Asp Tyr Pro Phe Lys Pro
 50 55 60

Pro Lys Ile Ala Phe Thr Thr Lys Ile Tyr His Pro Asn Ile Asn Ser
 65 70 75 80

Asn Gly Ser Ile Cys Leu Asp Ile Leu Arg Ser Gln Trp Ser Pro Ala
 85 90 95

Leu Thr Val Ser Lys Val Leu Leu Ser Ile Cys Ser Asp Leu Thr Asp
 100 105 110

Cys Asn Pro Asp Asp Pro Leu Val Pro Asp Ile Ala Gln Ile Tyr Lys
 115 120 125

Ser Asp Lys Glu Lys Tyr Asn Arg His Ala Arg Glu Trp Thr Gln Lys
 130 135 140

Tyr Ala Met
 145

<210> 18
 <211> 193
 <212> PRT
 <213> Human

<220>
 <221> MISC_FEATURE
 <222> (1)..(193)
 <223> UbCH6

<400> 18

Met Ser Asp Asp Asp Ser Arg Ala Ser Thr Ser Ser Ser Ser Ser Ser
 1 5 10 15

Ser Ser Asn Gln Gln Thr Glu Lys Glu Thr Asn Thr Pro Lys Lys Lys
 20 25 30

Glu Ser Lys Val Ser Met Ser Lys Asn Ser Lys Leu Leu Ser Thr Ser
 35 40 45

Ala Lys Arg Ile Gln Lys Glu Leu Ala Asp Ile Thr Leu Asp Pro Pro
 50 55 60

Pro Asn Cys Ser Ala Gly Pro Lys Gly Asp Asn Ile Tyr Glu Trp Arg
65 70 75 80

Ser Thr Ile Leu Gly Pro Pro Gly Ser Val Tyr Glu Gly Gly Val Phe
85 90 95

Phe Leu Asp Ile Thr Phe Thr Pro Glu Tyr Pro Phe Lys Pro Pro Lys
100 105 110

Val Thr Phe Arg Thr Arg Ile Tyr His Cys Asn Ile Asn Ser Gln Gly
115 120 125

Val Ile Cys Leu Asp Ile Leu Lys Asp Asn Trp Ser Pro Ala Leu Thr
130 135 140

Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Asp Leu Thr Asp Cys Asn
145 150 155 160

Pro Ala Asp Pro Leu Val Gly Ser Ile Ala Thr Gln Tyr Met Thr Asn
165 170 175

Arg Ala Glu His Asp Arg Met Ala Arg Gln Trp Thr Lys Arg Tyr Ala
180 185 190

Thr

<210> 19
<211> 154
<212> PRT
<213> Human

<220>
<221> MISC_FEATURE
<222> (1)..(154)
<223> UbCH7

<400> 19

Met Ala Ala Ser Arg Arg Leu Met Lys Glu Leu Glu Glu Ile Arg Lys
1 5 10 15

Cys Gly Met Lys Asn Phe Arg Asn Ile Gln Val Asp Glu Ala Asn Leu
20 25 30

Leu Thr Trp Gln Gly Leu Ile Val Pro Asp Asn Pro Pro Tyr Asp Lys
 35 40 45

Gly Ala Phe Arg Ile Glu Ile Asn Phe Pro Ala Glu Tyr Pro Phe Lys
 50 55 60

Pro Pro Lys Ile Thr Phe Lys Thr Lys Ile Tyr His Pro Asn Ile Asp
 65 70 75 80

Glu Lys Gly Gln Val Cys Leu Pro Val Ile Ser Ala Glu Asn Trp Lys
 85 90 95

Pro Ala Thr Lys Thr Asp Gln Val Ile Gln Ser Leu Ile Ala Asp Val
 100 105 110

Asn Asp Pro Gln Pro Glu His Pro Leu Arg Ala Asp Leu Ala Glu Glu
 115 120 125

Tyr Ser Lys Asp Arg Lys Lys Phe Cys Lys Asn Ala Glu Glu Phe Thr
 130 135 140

Lys Lys Tyr Gly Glu Lys Arg Pro Val Asp
 145 150

<210> 20
 <211> 152
 <212> PRT
 <213> Human

<220>
 <221> MISC_FEATURE
 <222> (1)..(152)
 <223> Ubch8

<400> 20

Met Ala Ser Met Arg Val Val Lys Glu Leu Glu Asp Leu Gln Lys Lys
 1 5 10 15

Pro Pro Pro Tyr Leu Arg Asn Leu Ser Ser Asp Asp Ala Asn Val Leu
 20 25 30

Val Trp His Ala Leu Leu Leu Pro Asp Gln Pro Pro Tyr His Leu Lys
 35 40 45

Ala Phe Asn Leu Arg Ile Ser Phe Pro Pro Glu Tyr Pro Phe Lys Pro
 50 55 60

Pro Met Ile Lys Phe Thr Thr Lys Ile Tyr His Pro Asn Val Asp Glu
 65 70 75 80

Asn Gly Gln Ile Cys Leu Pro Ile Ile Ser Ser Glu Asn Trp Lys Pro
 85 90 95

Cys Thr Lys Thr Cys Gln Val Leu Glu Ala Leu Asn Val Asp Val Asn
 100 105 110

Arg Pro Asn Ile Arg Glu Pro Leu Arg Met Asp Leu Ala Asp Leu Leu
 115 120 125

Thr Gln Asn Pro Glu Leu Phe Arg Lys Asn Ala Glu Glu Phe Thr Leu
 130 135 140

Arg Phe Gly Val Asp Arg Pro Ser
 145 150

<210> 21
 <211> 170
 <212> PRT
 <213> Human

<220>
 <221> MISC_FEATURE
 <222> (1)..(170)
 <223> UBE2G

<400> 21

Met Thr Glu Leu Gln Ser Ala Leu Leu Leu Arg Arg Gln Leu Ala Glu
 1 5 10 15

Leu Asn Lys Asn Pro Val Glu Gly Phe Ser Ala Gly Leu Ile Asp Asp
 20 25 30

Asn Asp Leu Tyr Arg Trp Glu Val Leu Ile Ile Gly Pro Pro Asp Thr
 35 40 45

Leu Tyr Glu Gly Gly Val Phe Lys Ala His Leu Thr Phe Pro Lys Asp
 50 55 60

Tyr Pro Leu Arg Pro Pro Lys Met Lys Phe Ile Thr Glu Ile Trp His
65 70 75 80

Pro Asn Val Asp Lys Asn Gly Asp Val Cys Ile Ser Ile Leu His Glu
85 90 95

Pro Gly Glu Asp Lys Tyr Gly Tyr Glu Lys Pro Glu Glu Arg Trp Leu
100 105 110

Pro Ile His Thr Val Glu Thr Ile Met Ile Ser Val Ile Ser Met Leu
115 120 125

Ala Asp Pro Asn Gly Asp Ser Pro Ala Asn Val Asp Ala Ala Lys Glu
130 135 140

Trp Arg Glu Asp Arg Asn Gly Glu Phe Lys Arg Lys Val Ala Arg Cys
145 150 155 160

Val Arg Lys Ser Gln Glu Thr Ala Phe Glu
165 170

<210> 22
<211> 183
<212> PRT
<213> Human

<220>
<221> MISC_FEATURE
<222> (1)..(183)
<223> UBC(8)

<400> 22

Met Ser Ser Pro Ser Pro Gly Lys Arg Arg Met Asp Thr Asp Val Val
1 5 10 15

Lys Leu Ile Glu Ser Lys His Glu Val Thr Ile Leu Gly Gly Leu Asn
20 25 30

Glu Phe Val Val Lys Phe Tyr Gly Pro Gln Gly Thr Pro Tyr Glu Gly
35 40 45

Gly Val Trp Lys Val Arg Val Asp Leu Pro Asp Lys Tyr Pro Phe Lys
50 55 60

Ser Pro Ser Ile Gly Phe Met Asn Lys Ile Phe His Pro Asn Ile Asp
65 70 75 80

Glu Ala Ser Gly Thr Val Cys Leu Asp Val Ile Asn Gln Thr Trp Thr
85 90 95

Ala Leu Tyr Asp Leu Thr Asn Ile Phe Glu Ser Phe Leu Pro Gln Leu
100 105 110

Leu Ala Tyr Pro Asn Pro Ile Asp Pro Leu Asn Gly Asp Ala Ala Ala
115 120 125

Met Tyr Leu His Arg Pro Glu Glu Tyr Lys Gln Lys Ile Lys Glu Tyr
130 135 140

Ile Gln Lys Tyr Ala Thr Glu Glu Ala Leu Lys Glu Gln Glu Glu Gly
145 150 155 160

Thr Gly Asp Ser Ser Ser Glu Ser Ser Met Ser Asp Phe Ser Glu Asp
165 170 175

Glu Ala Gln Asp Met Glu Leu
180

<210> 23
<211> 158
<212> PRT
<213> Human

<220>
<221> MISC_FEATURE
<222> (1)..(158)
<223> UBC9

<400> 23

Met Ser Gly Ile Ala Leu Ser Arg Leu Ala Gln Glu Arg Lys Ala Trp
1 5 10 15

Arg Lys Asp His Pro Phe Gly Phe Val Ala Val Pro Thr Lys Asn Pro
20 25 30

Asp Gly Thr Met Asn Leu Met Asn Trp Glu Cys Ala Ile Pro Gly Lys
35 40 45

Lys Gly Thr Pro Trp Glu Gly Gly Leu Phe Lys Leu Arg Met Leu Phe
 50 55 60

Lys Asp Asp Tyr Pro Ser Ser Pro Pro Lys Cys Lys Phe Glu Pro Pro
 65 70 75 80

Leu Phe His Pro Asn Val Tyr Pro Ser Gly Thr Val Cys Leu Ser Ile
 85 90 95

Leu Glu Glu Asp Lys Asp Trp Arg Pro Ala Ile Thr Ile Lys Gln Ile
 100 105 110

Leu Leu Gly Ile Gln Glu Asp Leu Asn Glu Pro Asn Ile Gln Asp Pro
 115 120 125

Ala Gln Ala Glu Ala Tyr Thr Ile Tyr Cys Gln Asn Arg Val Glu Tyr
 130 135 140

Glu Lys Arg Val Arg Ala Gln Ala Lys Lys Phe Ala Pro Ser
 145 150 155

<210> 24
 <211> 180
 <212> PRT
 <213> Human

<220>
 <221> MISC_FEATURE
 <222> (1)..(180)
 <223> UBCH10

<400> 24

Met Ala Ser Gln Asn Arg Asp Pro Ala Ala Thr Ser Val Ala Ala Ala
 1 5 10 15

Ala Arg Lys Gly Ala Glu Pro Ser Gly Gly Ala Ala Arg Gly Pro Val
 20 25 30

Gly Lys Arg Leu Gln Gln Glu Leu Met Thr Leu Met Met Ser Gly Asp
 35 40 45

Lys Gly Ile Ser Ala Phe Pro Glu Ser Asp Asn Leu Phe Lys Trp Val
 50 55 60

Gly Thr Ile His Gly Ala Ala Gly Thr Val Tyr Glu Asp Leu Arg Tyr
 65 70 75 80

Lys Leu Ser Leu Glu Phe Pro Ser Gly Tyr Pro Tyr Asn Ala Pro Thr
 85 90 95

Val Lys Phe Leu Thr Pro Cys Tyr His Pro Asn Val Asp Thr Gln Gly
 100 105 110

Asn Ile Cys Leu Asp Ile Leu Lys Glu Lys Trp Ser Ala Leu Tyr Asp
 115 120 125

Val Arg Thr Ile Leu Leu Ser Ile Gln Ser Asp Leu Gly Glu Pro Asn
 130 135 140

Ile Asp Ser Pro Leu Asn Thr His Ala Ala Glu Leu Trp Lys Asn Pro
 145 150 155 160

Thr Ala Phe Lys Lys Tyr Leu Gln Glu Thr Tyr Ser Lys Gln Val Thr
 165 170 175

Ser Gln Glu Pro
 180

<210> 25
 <211> 152
 <212> PRT
 <213> Human

<220>
 <221> MISC_FEATURE
 <222> (1)..(152)
 <223> UBC 13

<400> 25

Met Ala Gly Leu Pro Arg Arg Ile Ile Lys Glu Thr Gln Arg Leu Leu
 1 5 10 15

Ala Glu Pro Val Pro Gly Ile Lys Ala Glu Pro Asp Glu Ser Asn Ala
 20 25 30

Arg Tyr Phe His Val Val Ile Ala Gly Pro Gln Asp Ser Pro Phe Glu
 35 40 45

Gly Gly Thr Phe Lys Leu Glu Leu Phe Leu Pro Glu Glu Tyr Pro Met
 50 55 60

Ala Ala Pro Lys Val Arg Phe Met Thr Lys Ile Tyr His Pro Asn Val
 65 70 75 80

Asp Lys Leu Gly Arg Ile Cys Leu Asp Ile Leu Lys Asp Glu Trp Ser
 85 90 95

Pro Ala Leu Gln Ile Arg Thr Val Leu Leu Ser Ile Gln Ala Asp Leu
 100 105 110

Ser Ala Pro Asn Pro Asp Asp Pro Leu Ala Asn Asp Val Ala Glu Gln
 115 120 125

Trp Lys Thr Asn Glu Ala Gln Ala Ile Glu Thr Ala Arg Ala Trp Thr
 130 135 140

Arg Leu Tyr Ala Met Asn Asn Ile
 145 150

<210> 26

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Tryptic peptide sequence for p60

<220>

<221> MISC_FEATURE

<222> (11)..(13)

<223> Amino acids 11 and 13 are Xaa wherein Xaa = any amino acid.

<400> 26

Phe Thr Val Val Ala Thr Gln Leu Pro Glu Xaa Thr Xaa Leu
 1 5 10

<210> 27

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Tryptic peptide sequence for p60

<400> 27

Glu His Phe Gln Ser Tyr Asp Leu Asp His Met Glu
1 5 10

<210> 28

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Tryptic peptide sequence for p60

<400> 28

Gln Thr Pro Ser Phe Trp Ile Leu Ala
1 5

<210> 29

<211> 24

<212> DNA

<213> Human

<400> 29

gcaggatgat caagctgttc tcgc

24

<210> 30

<211> 24

<212> DNA

<213> Human

<400> 30

cgtggcgggg gtgggtatgc gccca

24

<210> 31

<211> 33

<212> DNA

<213> Human

<400> 31

cgggaattcc atatgatcaa gctgttctcg ctg

33

<210> 32

<211> 33

<212> DNA

<213> Human

<400> 32

cgcaccaagct tctatttcag gcagcgctca aag

33

<210> 33
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> N-terminus of NCE1

<400> 33

Met His His His His His His
 1 5

<210> 34
 <211> 24
 <212> PRT
 <213> Human

<400> 34

His Pro Asn Ile Thr Glu Thr Ile Cys Leu Ser Leu Leu Arg Glu His
 1 5 10 15

Ser Ile Asp Gly Thr Gly Trp Ala
 20

<210> 35
 <211> 20
 <212> DNA
 <213> Human

<400> 35
 agcccagggt aaaggcagca

20

<210> 36
 <211> 20
 <212> DNA
 <213> Human

<400> 36
 catgtagag acaaactgta

20

<210> 37
 <211> 31

<212> DNA
<213> Human

<400> 37
gggaattcca tatgctaacg ctagcaagta a

31

<210> 38
<211> 28
<212> DNA
<213> Human

<400> 38
ccatcgattc atctggcata acgtttga

28